

Figure 1 (SEQ ID NO:724)

85P1B3 SSH sequence and GenBank homology to OIP5

GATCAGAGGACACATGGGACTCTGCATCTTAATTCCTAAATTTACAGTCAAAGACATTTTCAG
 AGATAAGTATTATGAATTCAATAAGAATCTAAAGTAAGTTCTTAAGGCAAATAGCTATAAAA
 GAGAAGAATCCTTAGTCTCTCATCTTCTAAAAACAGCTTCACAAATAATTTGGAAAATCAGCC
 TAAAGGTAAATAGAACTGCATTTCCCTCCATTCTTGAAGCCAATCTTTTCAAGAAATGAC
 TAAGCAGCACCTGTTGTTGAAGACAGCAATAAAGCCTGAACCTGACACTCAAGCTTTGGTACA
 GGATC

gb|AF025441.1|AF025441 Homo sapiens Opa-interacting protein... 632 e-179
 gb|AF158642.1|AF158642 Homo sapiens metalloproteinase-disin... 42 0.12
 gb|AC005075.2|AC005075 Homo sapiens clone RG219E16, complet... 42 0.12
 emb|AL096773.6|HS1000E10 Human DNA sequence from clone 1000... 40 0.48

>gb|AF025441.1|AF025441 Homo sapiens Opa-interacting protein OIP5 mRNA, partial cds
 Length = 1197

Score = 632 bits (319), Expect = e-179
 Identities = 319/319 (100%)
 Strand = Plus / Minus

Query: 1 gatcagaggacacatgggactctgcatcttaattcctaaatttacagtcaaagacatttt 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Sbjct: 1013 gatcagaggacacatgggactctgcatcttaattcctaaatttacagtcaaagacatttt 954

Query: 61 cagagataagtattatgaattcaataagaatctaaagtaagttcttaaggcaaatagcta 120
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Sbjct: 953 cagagataagtattatgaattcaataagaatctaaagtaagttcttaaggcaaatagcta 894

Query: 121 taaaagagaagaatccttagtctctcatcttctaaaaacagcttcacaaataatttgga 180
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Sbjct: 893 taaaagagaagaatccttagtctctcatcttctaaaaacagcttcacaaataatttgga 834

Query: 181 aatcagcctaaaggtaaataagaaactgcatttcccctccattcttgaagccaatctttt 240
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Sbjct: 833 aatcagcctaaaggtaaataagaaactgcatttcccctccattcttgaagccaatctttt 774

Query: 241 caagaaatgactaagcagcacctgtgtgtgaagacagcaataaagcctgaacctgacact 300
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Sbjct: 773 caagaaatgactaagcagcacctgtgtgtgaagacagcaataaagcctgaacctgacact 714

Query: 301 caagctttggtacaggatc 319 (SEQ ID NO:725)
 ||||||||||||||||
 Sbjct: 713 caagctttggtacaggatc 695 (SEQ ID NO:726)

Figure 2

cdNA Sequence and ORF of 85P1B3/OIP5 clone A
(SEQ ID NO:727)

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      9      18      27      36      45      54
5' GGC TGC GGG AAG ATG GCG GCT CAG CCG CTG CGG CAT CGC TCA CGT TGT GCA ACG
   (SEQ ID NO:728) M  A  A  Q  P  L  R  H  R  S  R  C  A  T
      63      72      81      90      99     108
CCG CCC CGG GGG GAC TTT TGT GGT GGC ACT GAG AGG GCG ATT GAC CAA GCT TCT
   P  P  R  G  D  F  C  G  G  T  E  R  A  I  D  Q  A  S
      117     126     135     144     153     162
TTT ACG ACC TCC ATG GAG TGG GAT ACG CAG GTG GTG AAG GGG TCC TCG CCG CTC
   F  T  T  S  M  E  W  D  T  Q  V  V  K  G  S  S  P  L
      171     180     189     198     207     216
GGC CCC GCA GGG CTG GGG GCT GAG GAG CCA GCC GCC GGC CCG CAG CTG CCG TCT
   G  P  A  G  L  G  A  E  E  P  A  A  G  P  Q  L  P  S
      225     234     243     252     261     270
TGG CTG CAG CCT GAG AGG TGC GCT GTG TTC CAG TGC GCA CAG TGT CAC GCA GTG
   W  L  Q  P  E  R  C  A  V  F  Q  C  A  Q  C  H  A  V
      279     288     297     306     315     324
CTC GCC GAC TCG GTG CAC CTC GCC TGG GAC CTG TCG CGG TCC CTC GGG GCC GTG
   L  A  D  S  V  H  L  A  W  D  L  S  R  S  L  G  A  V
      333     342     351     360     369     378
GTC TTC TCC AGA GTT ACA AAT AAC GTC GTT TTG GAA GCG CCC TTC CTA GTT GGC
   V  F  S  R  V  T  N  N  V  V  L  E  A  P  F  L  V  G
      387     396     405     414     423     432
ATT GAA GGT TCA CTC AAA GGC AGT ACT TAC AAC CTT TTA TTC TGT GGT TCT TGT
   I  E  G  S  L  K  G  S  T  Y  N  L  L  F  C  G  S  C
      441     450     459     468     477     486
GGG ATT CCC GTT GGT TTC CAT CTG TAT TCT ACC CAT GCT GCC CTG GCT GCC TTG
   G  I  P  V  G  F  H  L  Y  S  T  H  A  A  L  A  A  L
      495     504     513     522     531     540
AGA GGT CAC TTC TGC CTT TCC AGT GAC AAA ATG GTG TGC TAT CTC TTA AAA ACA
   R  G  H  F  C  L  S  S  D  K  M  V  C  Y  L  L  K  T
      549     558     567     576     585     594
AAA GCC ATA GTA AAT GCA TCA GAG ATG GAT ATT CAA AAT GTT CCT CTA TCA GAA
   K  A  I  V  N  A  S  E  M  D  I  Q  N  V  P  L  S  E
      603     612     621     630     639     648
AAG ATT GCA GAG CTG AAA GAG AAG ATA GTG CTA ACG CAC AAT CGC TTA AAA TCA
   K  I  A  E  L  K  E  K  I  V  L  T  H  N  R  L  K  S

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AAA AAA AAA AAA AAA AAA AA 3'

Figure 3

85P1B3/OIP5 protein sequence. (SEQ ID NO:729)

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1 MAAQPLRHRS RCATPFRGDF CGGTERAIDQ ASFTTSMEDW TQVVKGSSPL GPAGLGAEED
61 AAGPQLPSWL QPERCAVFQC AQCHAVLADS VHAWDLRS LGAVVFSRVT NNVVLEAPFL
121 VGIEGSLKGS TYNLLFCGSC GIPVGFHLYS THAALAALRG HFCLSSDKMV CYLLKTKAIV
181 NASEMDIQNV PLSEKIAELK EKIVLTHNRL KSLMKILSEV TPDQSKPEN*
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Figure 4

Alignment of 85P1B3 with OIP5.

>gi|2815610|gb|AAC39561.1|(AF025441) Opa-interacting protein OIP5 [Homo sapiens]
Length = 231

Score = 462 bits (1189), Expect = e-130

Identities = 229/229 (100%), Positives = 229/229 (100%)

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85P1B3: 1  MAAQPLRHRSRCATPPRGDFCGGTERAIDQASFTTSMEWDTQVVKGSSPLGPAGLGAEPP 60
      MAAQPLRHRSRCATPPRGDFCGGTERAIDQASFTTSMEWDTQVVKGSSPLGPAGLGAEPP
OIP5: 3  MAAQPLRHRSRCATPPRGDFCGGTERAIDQASFTTSMEWDTQVVKGSSPLGPAGLGAEPP 62

85P1B3: 61  AAGPQLPSWLQPERCAVFQCAQCHAVLADSVHLAWDLRSRLGAVVFSRVTTNNVVLEAPFL 120
      AAGPQLPSWLQPERCAVFQCAQCHAVLADSVHLAWDLRSRLGAVVFSRVTTNNVVLEAPFL
OIP5: 63  AAGPQLPSWLQPERCAVFQCAQCHAVLADSVHLAWDLRSRLGAVVFSRVTTNNVVLEAPFL 122

85P1B3:121  VGIEGSLKGSTYNLLFCGSCGIPVGFHLYSTHAALAALRGHFCLSSDKMVCYLLKTKAIV 180
      VGIEGSLKGSTYNLLFCGSCGIPVGFHLYSTHAALAALRGHFCLSSDKMVCYLLKTKAIV
OIP5: 123  VGIEGSLKGSTYNLLFCGSCGIPVGFHLYSTHAALAALRGHFCLSSDKMVCYLLKTKAIV 182

85P1B3:181  NASEMDIQNVPLSEKIAELKEKIVLTHNRLKSLMKILSEVTPDQSKPEN 229 (SEQ ID NO:730)
      NASEMDIQNVPLSEKIAELKEKIVLTHNRLKSLMKILSEVTPDQSKPEN
OIP5: 183  NASEMDIQNVPLSEKIAELKEKIVLTHNRLKSLMKILSEVTPDQSKPEN 231 (SEQ ID NO:731)
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Fig. 21A

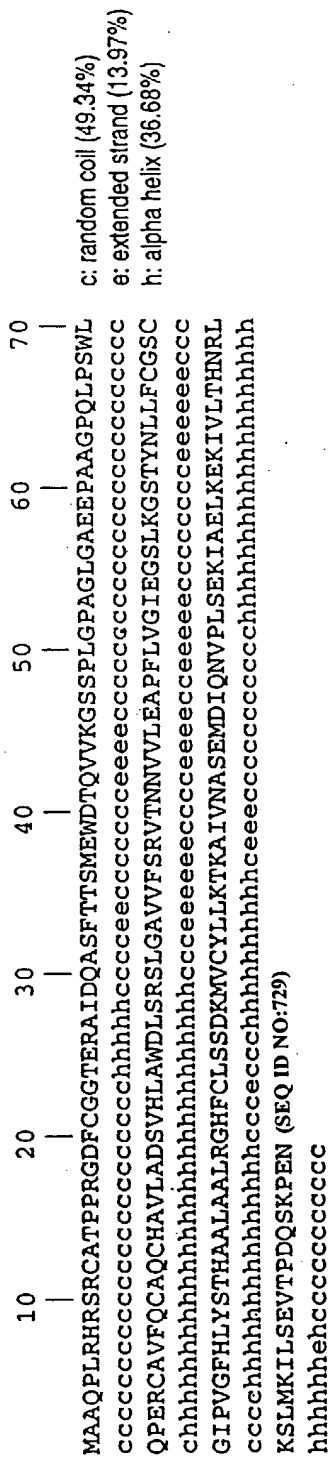
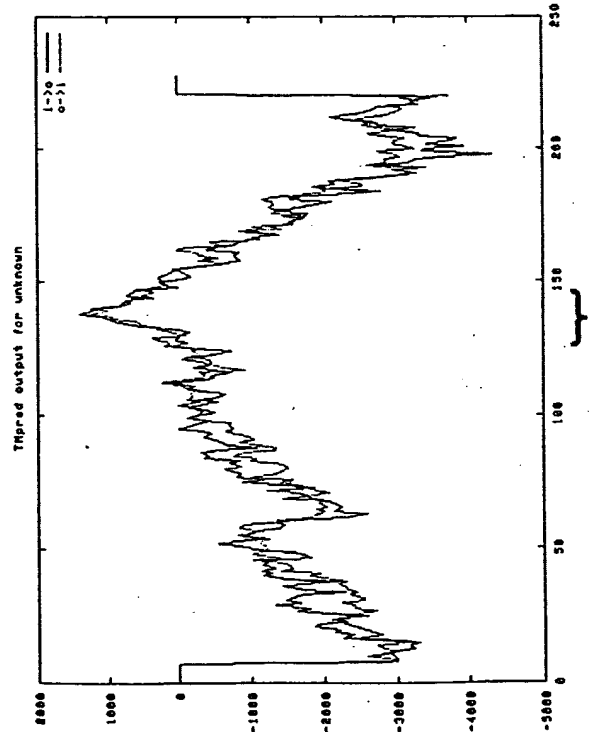
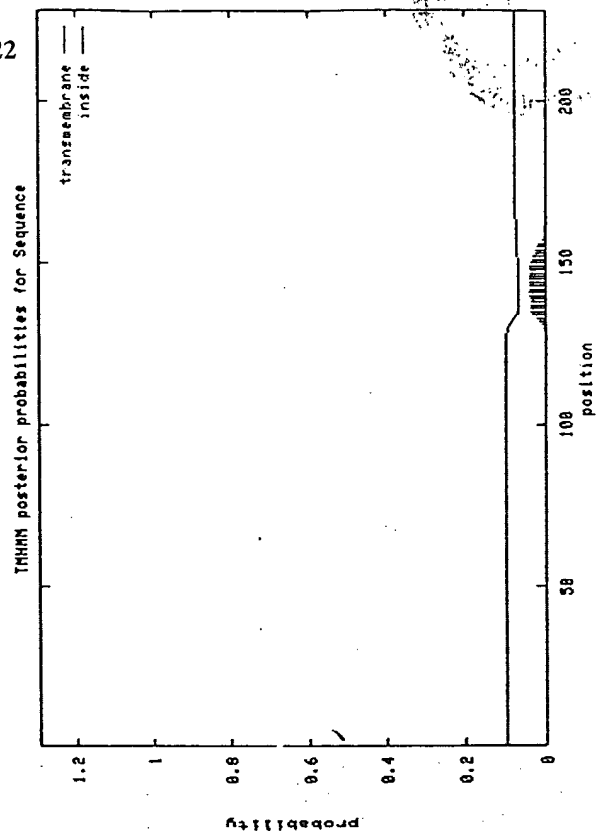


Fig. 21B



1 transmembrane from amino acids 129-149

Fig. 21C



No transmembrane domains, soluble protein